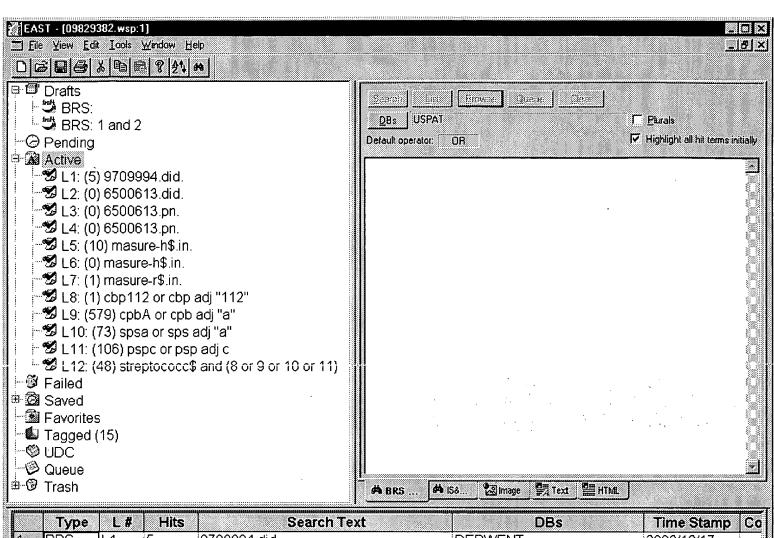
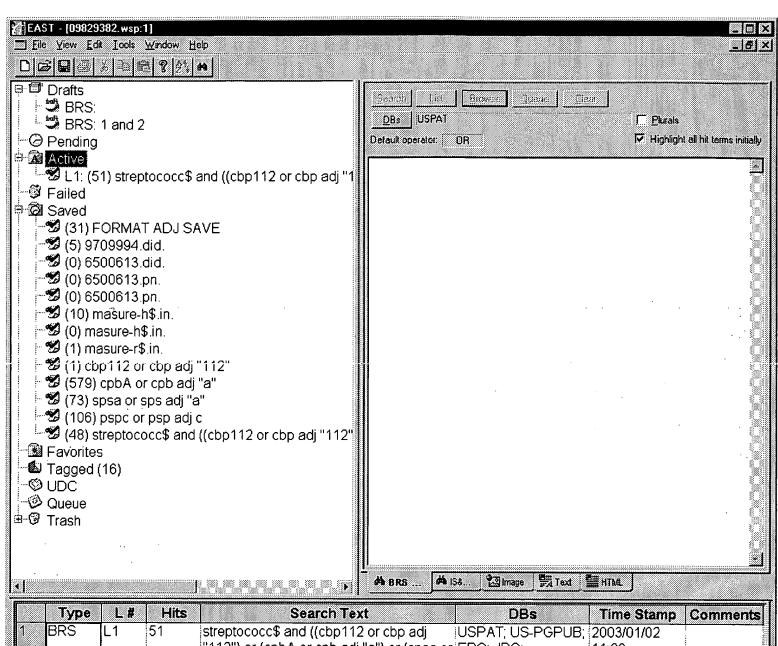
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•		adj "a") or (spsa or sps adj "a") or (pspc or psp adj c))	US-PGPUB;	2000/10/00 12:00
		day a yor topoa or ope aay a yor toope or pop aay oy	EPO; JPO;	
			DERWENT	
8	71	streptococc\$ and (pbca or hic)	USPAT;	2003/10/08 12:35
'	, ,	streptococcu and (poca of file)	US-PGPUB;	2003/10/06 12.33
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_	51	streptococc\$ and ((cbp112 or cbp adj "112") or (cpbA or cpb		2002/40/09 42:47
-	ان		USPAT;	2003/10/08 12:17
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			EPO; JPO;	
		stronto 0000 and //shr440 == == == : !!440!!\ == / = !	DERWENT	0000/40/00 40 45
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- '	43	streptococc\$ and (pbca or hic)	USPAT;	2003/10/08 12:18
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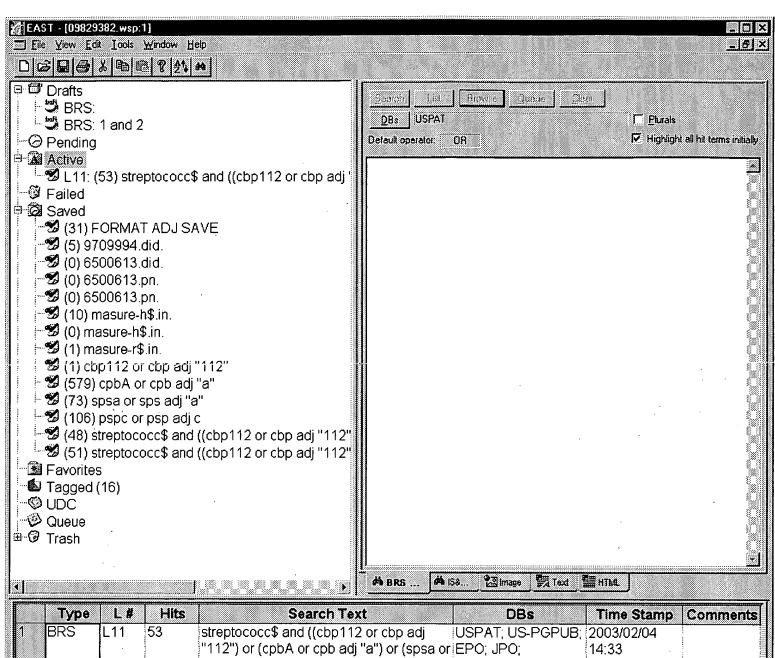


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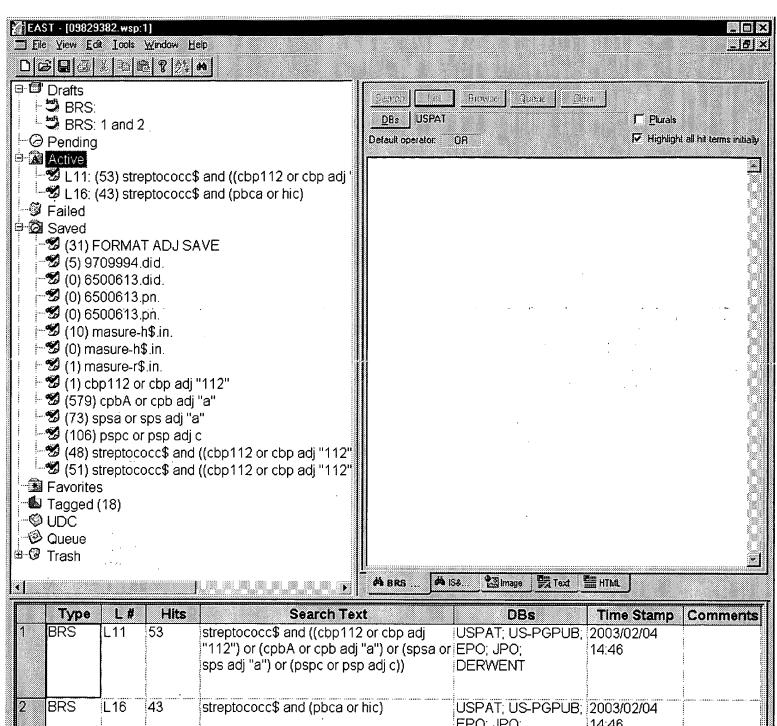
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				sps adj "a") or (pspc or psp adj c))	DERVVEINI		
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	Type	L#	Hits	Search Text	DBs	Time Stamp	Comments
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4/7/11 DIALOG(R)File 155:MEDLINE(R)

09610290 98010350 PMID: 9350867

SpsA, a novel pneumococcal surface protein with specific binding to secretory immunoglobulin A and secretory component.

Hammerschmidt S; Talay S R; Brandtzaeg P; Chhatwal G S

Department of Microbial Pathogenesis, GBF-National Research Centre for Biotechnology, Braunschweig, Germany.

Molecular microbiology (ENGLAND) Sep 1997, 25 (6) p1113-24, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM Record type: Completed

The interaction of pathogenic bacteria with host serum and matrix proteins is a common strategy to enhance their virulence. Streptococcus pneumoniae colonizes the human upper respiratory tract in healthy individuals and is also able to cause invasive diseases. Here, we describe a novel pneumococcal surface protein, SpsA, capable of binding specifically to human secretory immunoglobulin A (SIgA). The dissociation constant of SIGA binding to SpsA was $9.3 \times 10(-9)$ M. Free secretory component (SC) also binds to S. pneumoniae, whereas serum IgA does not, suggesting that pneumococcal binding to SIgA is mediated by the SC. To our knowledge, this is the first defined interaction of SC with a prokaryotic protein. The spsA gene encodes a polypeptide of 523 amino acids with a predicted molecular mass of 59 151 Da. The SIgA- or SC-binding domain is located in the N-terminal part of SpsA and exhibits no significant homology to any other proteins. The purified SIgA-binding domain of SpsA could completely inhibit the binding of SIgA to pneumococci. SpsA was expressed by 73% of the tested S. pneumoniae isolates and was substantially conserved between different serotypes. The interaction between S. pneumoniae and SC via SpsA represents a novel biological interaction that might increase virulence by the impairment of bacterial clearance.

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A150/9709994

Also 6,500,613 (155ming 12/31/02)

13151920 21888621 PMID: 11891047

Allelic variation in the highly polymorphic locus pspC of Streptococcus pneumoniae.

Iannelli Francesco; Oggioni Marco R; Pozzi Gianni

Laboratory of Molecular Microbiology and Biotechnology, Sezione di Microbiologia, Dipartimento di Biologia Molecolare, Universita di Siena, 53100, Siena, Italy.

Gene (Netherlands) Feb 6 2002, 284 (1-2) p63-71, ISSN 0378-1119 Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM Record type: Completed

PspC, also called SpsA, CbpA, PbcA, and Hic, is a surface protein of studied for its antigenic properties, its Streptococcus pneumoniae capability to bind secretory IgA, C3 and complement factor H, and its activity as an adhesin. In this work we characterized the pspC locus of 43 pneumococcal strains by DNA sequencing of PCR fragments. Using PCR primers designed on two unrelated open reading frames, flanking the pspC locus, it was possible to amplify the pspC locus of each of the 43 strains of S. pneumoniae. In 37 out of 43 strains there was a single copy of the pspC gene, while two tandem copies of pspC were found in the other six strains. The sequence of the pspC locus was different in each of the 43 strains. Insertion sequences were found in the pspC locus of 11 out of 43 strains. Analysis of the deduced amino acid sequence of the PspC variants showed a common organization of the molecules: (i) a 37 amino acid leader peptide which is conserved in all proteins, (ii) an N-terminal portion which is essentially alpha-helical, and is the result of assembly of eight major sequence blocks, (iii) a proline-rich region, and (iv) a C-terminal anchor responsible for the cell surface attachment. By sequence comparison we identified 11 major groups of PspC proteins. Proteins within one group displayed only minor variations of the amino acid sequence. An unexpected finding was that PspC variants could differ in the anchor sequence. While 32 of the PspC proteins displayed the typical choline binding domain of pneumococcal surface proteins, 17 other PspCs showed the LPXTG motif, which is typical of surface proteins of other gram-positive bacteria. This major difference in the anchor region was also observed in the adjacent proline-rich regions which differed considerably in size and composition.

Record Date Created: 20020313